

10/537201

SEQUENCE LISTING

<110> Van der Geize, Robert
Hessels, Gerda
Dijkhuizen, Lubbert
Van der Meijden, Peter

<120> New expression system from Rhodococcus

<130> 2002.744US

<140> 10/537,201

<141> 2005-06-02

<150> PCT/EP03/050928

<151> 2003-12-02

<150> EP02080054.6

<151> 2002-12-03

<160> 13

<170> PatentIn Ver. 2.1

<210> 1

<211> 1543

<212> DNA

<213> Rhodococcus erythropolis

<220>

<221> CDS

<222> (1)..(1533)

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acg atc gtc ctc gag aaa acc gat cgt ttc ggc ggg acc tcc gcc tac	144
Thr Ile Val Leu Glu Lys Thr Asp Arg Phe Gly Gly Thr Ser Ala Tyr	
35 40 45	
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Ser Gly Ala Ser Ile Trp Leu Pro Gly Thr Gln Val Gln Glu Arg Ala	
50 55 60	
gga ctt ccc gac tcg acc gag aat gcc cgc acc tat ctg cgc gcg ttg	240
Gly Leu Pro Asp Ser Thr Glu Asn Ala Arg Thr Tyr Leu Arg Ala Leu	
65 70 75 80	
ctc ggt gac gcc gag tcc gag cgc cag gac gcc tac gtc gag acc gct	288
Leu Gly Asp Ala Glu Ser Glu Arg Gln Asp Ala Tyr Val Glu Thr Ala	
85 90 95	
ccc gct gtc gtc gct cta ctc gag cag aac ccg aac atc gaa ttc gag	336
Pro Ala Val Val Ala Leu Leu Glu Gln Asn Pro Asn Ile Glu Phe Glu	
100 105 110	

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Asp	His	Ala	Pro	Gly	Pro	Met	Ile	Gly	Gly	Arg	Ala	Leu	Ile	Gly	Arg	
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Gln	Ala	Gly	Thr	Pro	Gly	Lys	Ala	Ile	Trp	Ser	Met	Gly	Pro	Phe	Gly	
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Val Gly Ala Asp Thr Leu Glu Glu Leu Ala Ala Lys Thr Gly Leu Pro	
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Ala Asp Ala Leu Arg Ser Thr Val Glu Lys Phe Asn Asp Ala Ala Lys	
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Glu Asn Gly Pro Phe Tyr Ala Ala Arg Ile Val Leu Ser Asp Leu Gly	
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Thr Lys Gly Gly Leu Val Thr Asp Val Asn Gly Arg Val Leu Arg Ala	
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Asp Gly Ser Ala Ile Asp Gly Leu Tyr Ala Ala Gly Asn Thr Ser Ala	
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 35 40 45
 Ser Gly Ala Ser Ile Trp Leu Pro Gly Thr Gln Val Gln Glu Arg Ala
 50 55 60

Gly	Leu	Pro	Asp	Ser	Thr	Glu	Asn	Ala	Arg	Thr	Tyr	Leu	Arg	Ala	Leu	65	70	75	80
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Pro	Ala	Val	Val	Ala	Leu	Leu	Glu	Gln	Asn	Pro	Asn	Ile	Glu	Phe	Glu	100	105	110	
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Gly	Arg	Ser	Ile	Asn	Pro	Leu	Asp	Leu	Asp	Pro	Ala	Asp	Ile	Gly	Asp	130	135	140	
Leu	Ala	Gly	Lys	Val	Arg	Pro	Glu	Leu	Asp	Gln	Asp	Arg	Thr	Gly	Gln	145	150	155	160
Asp	His	Ala	Pro	Gly	Pro	Met	Ile	Gly	Gly	Arg	Ala	Leu	Ile	Gly	Arg	165	170	175	
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Ser	Val	Leu	Thr	Ser	Leu	Ile	Val	Glu	Asp	Gly	Arg	Val	Val	Gly	Ala	195	200	205	
Glu	Val	Glu	Ser	Gly	Gly	Glu	Thr	Gln	Arg	Ile	Lys	Ala	Asn	Arg	Gly	210	215	220	
Val	Leu	Met	Ala	Ala	Gly	Gly	Ile	Glu	Gly	Asn	Ala	Glu	Met	Arg	Glu	225	230	235	240
Gln	Ala	Gly	Thr	Pro	Gly	Lys	Ala	Ile	Trp	Ser	Met	Gly	Pro	Phe	Gly	245	250	255	
Ala	Asn	Thr	Gly	Asp	Ala	Ile	Ser	Ala	Gly	Ile	Ala	Val	Gly	Gly	Ala	260	265	270	
Thr	Ala	Leu	Leu	Asp	Gln	Ala	Trp	Phe	Cys	Pro	Gly	Val	Glu	Gln	Pro	275	280	285	
Asp	Gly	Ser	Ala	Ala	Phe	Met	Val	Gly	Val	Arg	Gly	Gly	Leu	Val	Val	290	295	300	
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Phe	Gly	Arg	Ala	Met	Asp	Ala	His	Asp	Asp	Asn	Gly	Ser	Ala	Val	Pro	325	330	335	
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Cys	Ile	Pro	Asn	Thr	Ala	Pro	Ala	Lys	His	Leu	Glu	Ala	Gly	Thr	Trp	355	360	365	
Val	Gly	Ala	Asp	Thr	Leu	Glu	Glu	Leu	Ala	Ala	Lys	Thr	Gly	Leu	Pro	370	375	380	
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Glu Asn Gly Pro	Phe Tyr Ala Ala	Arg Ile Val Leu	Ser Asp Leu Gly
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Thr Lys Gly Gly	Leu Val Thr Asp Val	Asn Gly Arg	Val Leu Arg Ala
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Asp Gly Ser Ala	Ile Asp Gly Leu Tyr	Ala Ala Gly Asn Thr	Ser Ala
465	470	475	480
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20 25 30				
gcc gcc gaa ttg ggg acc gag aaa gaa ctc tca cgg gtt cag atg cac	144			
Ala Ala Glu Leu Gly Thr Glu Lys Glu Leu Ser Arg Val Gln Met His				
35 40 45				
gaa gtt gcc aag cgg gca ggc gtg gcc atc ggc act ctc tac cgc tat	192			
Glu Val Ala Lys Arg Ala Gly Val Ala Ile Gly Thr Leu Tyr Arg Tyr				
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ttc cct tcg aag acg cac ctc ttc gtc gct gtg atg gtc gag cag atc	240			
Phe Pro Ser Lys Thr His Leu Phe Val Ala Val Met Val Glu Gln Ile				
65 70 75 80				
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Asp Gln Ile Gly Asp Ser Phe Ala Lys His Gln Val Gln Ser Ala Asn				
85 90 95				
ccg cag gac gcc gtg tac gag gtc ctg gtg cgc gcg act cgc ggg tta	336			
Pro Gln Asp Ala Val Tyr Glu Val Leu Val Arg Ala Thr Arg Gly Leu				
100 105 110				
ctg cgt cgg ccg gcc ctt tcg act gcg atg ctg cag tcg tcc agt acc	384			
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115 120 125				
gcc aac gtc gcg acg gtg ccg gac gtg ggc aag atc gat cgc ggc ttc	432			
Ala Asn Val Ala Thr Val Pro Asp Val Gly Lys Ile Asp Arg Gly Phe				
130 135 140				
cgg cag atc atc ctc gat gcg gcc ggg atc gag aac ccg acc gag gaa	480			
Arg Gln Ile Ile Leu Asp Ala Ala Gly Ile Glu Asn Pro Thr Glu Glu				
145 150 155 160				
gac aac acc ggg ttg cgt ctg ctg atg cag ctg tgg ttc ggg gtc atc	528			
Asp Asn Thr Gly Leu Arg Leu Leu Met Gln Leu Trp Phe Gly Val Ile				
165 170 175				
caa tcg tgc ctc aac ggt cga att tcc atc ccg gat gcg gag tac gac	576			
Gln Ser Cys Leu Asn Gly Arg Ile Ser Ile Pro Asp Ala Glu Tyr Asp				
180 185 190				
atc cgc aag ggg tgc gac ctg ctt ctg gtg aat ctc tca cga cac tga	624			
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<212> PRT

<213> Rhodococcus erythropolis

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Glu	Val	Ala	Lys	Arg	Ala	Gly	Val	Ala	Ile	Gly	Thr	Leu	Tyr	Arg	Tyr
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Phe	Pro	Ser	Lys	Thr	His	Leu	Phe	Val	Ala	Val	Met	Val	Glu	Gln	Ile
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Asp	Gln	Ile	Gly	Asp	Ser	Phe	Ala	Lys	His	Gln	Val	Gln	Ser	Ala	Asn
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Pro	Gln	Asp	Ala	Val	Tyr	Glu	Val	Leu	Val	Arg	Ala	Thr	Arg	Gly	Leu
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Leu	Arg	Arg	Pro	Ala	Leu	Ser	Thr	Ala	Met	Leu	Gln	Ser	Ser	Ser	Thr
			115					120					125		
Ala	Asn	Val	Ala	Thr	Val	Pro	Asp	Val	Gly	Lys	Ile	Asp	Arg	Gly	Phe
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Asp	Asn	Thr	Gly	Leu	Arg	Leu	Leu	Met	Gln	Leu	Trp	Phe	Gly	Val	Ile
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Gln	Ser	Cys	Leu	Asn	Gly	Arg	Ile	Ser	Ile	Pro	Asp	Ala	Glu	Tyr	Asp
			180					185					190		
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<220>
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

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<210> 9

<211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

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<210> 10
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 <220>
 <223> Description of Artificial Sequence:primer

 <400> 10
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<210> 11
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 <220>
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 <220>
 <223> Description of Artificial Sequence:primer

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 gccactagtt cactgcgctg ctctgcacg 30

SEQUENCE LISTING

<110> Van der Geize, Robert
Hessels, Gerda
Dijkhuizen, Lubbert
Van der Meijden, Peter

<120> New expression system from Rhodococcus

<130> 2002.744US

<140> 10/537,201

<141> 2005-06-02

<150> PCT/EP03/050928

<151> 2003-12-02

<150> EP02080054.6

<151> 2002-12-03

<160> 13

<170> PatentIn Ver. 2.1

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<211> 1543

<212> DNA

<213> Rhodococcus erythropolis

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<222> (1)..(1533)

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Gly Gly Ala Leu Thr Gly Ala Tyr Thr Ala Ala Ala Gln Gly Leu Thr	
20 25 30	
acg atc gtc ctc gag aaa acc gat cgt ttc ggc ggg acc tcc gcc tac	144
Thr Ile Val Leu Glu Lys Thr Asp Arg Phe Gly Gly Thr Ser Ala Tyr	
35 40 45	
tcg ggc gcc tcg atc tgg ctc cca ggt acc cag gtg cag gaa cgc gcc	192
Ser Gly Ala Ser Ile Trp Leu Pro Gly Thr Gln Val Gln Glu Arg Ala	
50 55 60	
gga ctt ccc gac tcg acc gag aat gcc cgc acc tat ctg cgc gcg ttg	240
Gly Leu Pro Asp Ser Thr Glu Asn Ala Arg Thr Tyr Leu Arg Ala Leu	
65 70 75 80	
ctc ggt gac gcc gag tcc gag cgc cag gac gcc tac gtc gag acc gct	288
Leu Gly Asp Ala Glu Ser Glu Arg Gln Asp Ala Tyr Val Glu Thr Ala	
85 90 95	
ccc gct gtc gtc gct cta ctc gag cag aac ccg aac atc gaa ttc gag	336
Pro Ala Val Val Ala Leu Leu Glu Gln Asn Pro Asn Ile Glu Phe Glu	
100 105 110	

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Gly	Arg	Ser	Ile	Asn	Pro	Leu	Asp	Leu	Asp	Pro	Ala	Asp	Ile	Gly	Asp	
	130					135					140					
ctc	gcc	ggc	aag	gtg	cgt	ccg	gaa	ctg	gac	caa	gac	cgc	acc	ggg	cag	480
Leu	Ala	Gly	Lys	Val	Arg	Pro	Glu	Leu	Asp	Gln	Asp	Arg	Thr	Gly	Gln	
145					150					155					160	
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225					230					235					240	
cag	gca	ggc	acc	ccc	ggc	aag	gcg	atc	tgg	agt	atg	ggg	ccc	ttc	ggc	768
Gln	Ala	Gly	Thr	Pro	Gly	Lys	Ala	Ile	Trp	Ser	Met	Gly	Pro	Phe	Gly	
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gcc	aac	acc	ggc	gac	gcg	atc	tct	gcc	ggg	att	gct	gtc	ggc	ggc	gca	816
Ala	Asn	Thr	Gly	Asp	Ala	Ile	Ser	Ala	Gly	Ile	Ala	Val	Gly	Gly	Ala	
			260					265					270			
aca	gcc	ttg	ctc	gat	cag	gcg	tgg	ttc	tgc	ccc	ggc	gtc	gag	cag	ccc	864
Thr	Ala	Leu	Leu	Asp	Gln	Ala	Trp	Phe	Cys	Pro	Gly	Val	Glu	Gln	Pro	
		275					280					285				
gac	ggc	agc	gcc	gcc	ttc	atg	gtc	ggc	gtt	cgc	ggg	ggg	ctc	gtc	gtc	912
Asp	Gly	Ser	Ala	Ala	Phe	Met	Val	Gly	Val	Arg	Gly	Gly	Leu	Val	Val	
	290					295					300					
gac	agc	gcc	ggg	gag	cgc	tac	ctc	aac	gag	tgc	ctt	ccg	tac	gac	cag	960
Asp	Ser	Ala	Gly	Glu	Arg	Tyr	Leu	Asn	Glu	Ser	Leu	Pro	Tyr	Asp	Gln	
305					310					315					320	
ttc	gga	cga	gcc	atg	gat	gct	cac	gac	gac	aac	ggg	tct	gcc	gtg	ccg	1008
Phe	Gly	Arg	Ala	Met	Asp	Ala	His	Asp	Asp	Asn	Gly	Ser	Ala	Val	Pro	
				325					330					335		
tgc	ttc	atg	atc	ttc	gac	tgc	cgc	gag	ggg	ggc	gga	ctg	ccc	gcc	atc	1056
Ser	Phe	Met	Ile	Phe	Asp	Ser	Arg	Glu	Gly	Gly	Gly	Leu	Pro	Ala	Ile	
			340					345					350			

tgc atc ccg aac acg gcg ccc gcc aag cac ctc gaa gcc gga acg tgg	1104
Cys Ile Pro Asn Thr Ala Pro Ala Lys His Leu Glu Ala Gly Thr Trp	
355 360 365	
gtc ggt gcc gac act ctc gaa gaa ctc gct gcc aag acc gga cta ccg	1152
Val Gly Ala Asp Thr Leu Glu Leu Ala Ala Lys Thr Gly Leu Pro	
370 375 380	
gcc gac gca ttg cgc agc act gtc gaa aag ttc aac gat gcc gca aaa	1200
Ala Asp Ala Leu Arg Ser Thr Val Glu Lys Phe Asn Asp Ala Ala Lys	
385 390 395 400	
ctg ggc gtc gac gaa gag ttc cat cgc ggc gaa gac ccg tac gac gcg	1248
Leu Gly Val Asp Glu Phe His Arg Gly Glu Asp Pro Tyr Asp Ala	
405 410 415	
ttc ttc tgc cca ccc aac ggc ggt gcg aat gcg gca ctg acg gcc atc	1296
Phe Phe Cys Pro Pro Asn Gly Gly Ala Asn Ala Ala Leu Thr Ala Ile	
420 425 430	
gag aac gga ccg ttc tac gcg gcc cgc atc gtc ctc agt gac ctc ggc	1344
Glu Asn Gly Pro Phe Tyr Ala Ala Arg Ile Val Leu Ser Asp Leu Gly	
435 440 445	
acc aag ggc gga ttg gtc acc gac gtc aac ggc cga gtc ctg cgt gct	1392
Thr Lys Gly Gly Leu Val Thr Asp Val Asn Gly Arg Val Leu Arg Ala	
450 455 460	
gac ggc agc gcc atc gac ggc ctg tac gcc gcc ggc aac acg agc gcg	1440
Asp Gly Ser Ala Ile Asp Gly Leu Tyr Ala Ala Gly Asn Thr Ser Ala	
465 470 475 480	
tca ctg agc ggc cgc ttc tac ccc ggc ccc gga gtt cca ctc ggc acg	1488
Ser Leu Ser Gly Arg Phe Tyr Pro Gly Pro Gly Val Pro Leu Gly Thr	
485 490 495	
gct atg gtc ttc tcg tac cga gca gct cag gac atg gcg aag taa	1533
Ala Met Val Phe Ser Tyr Arg Ala Ala Gln Asp Met Ala Lys	
500 505 510	
cgcagttcaa	1543

<210> 2
 <211> 510
 <212> PRT
 <213> Rhodococcus erythropolis

<400> 2
 Met Gln Asp Trp Thr Ser Glu Cys Asp Val Leu Val Val Gly Ser Gly
 1 5 10 15
 Gly Gly Ala Leu Thr Gly Ala Tyr Thr Ala Ala Ala Gln Gly Leu Thr
 20 25 30
 Thr Ile Val Leu Glu Lys Thr Asp Arg Phe Gly Gly Thr Ser Ala Tyr
 35 40 45
 Ser Gly Ala Ser Ile Trp Leu Pro Gly Thr Gln Val Gln Glu Arg Ala
 50 55 60

Gly	Leu	Pro	Asp	Ser	Thr	Glu	Asn	Ala	Arg	Thr	Tyr	Leu	Arg	Ala	Leu	65	70	75	80
Leu	Gly	Asp	Ala	Glu	Ser	Glu	Arg	Gln	Asp	Ala	Tyr	Val	Glu	Thr	Ala	85	90	95	
Pro	Ala	Val	Val	Ala	Leu	Leu	Glu	Gln	Asn	Pro	Asn	Ile	Glu	Phe	Glu	100	105	110	
Phe	Arg	Ala	Phe	Pro	Asp	Tyr	Tyr	Lys	Ala	Glu	Gly	Arg	Met	Asp	Thr	115	120	125	
Gly	Arg	Ser	Ile	Asn	Pro	Leu	Asp	Leu	Asp	Pro	Ala	Asp	Ile	Gly	Asp	130	135	140	
Leu	Ala	Gly	Lys	Val	Arg	Pro	Glu	Leu	Asp	Gln	Asp	Arg	Thr	Gly	Gln	145	150	155	160
Asp	His	Ala	Pro	Gly	Pro	Met	Ile	Gly	Gly	Arg	Ala	Leu	Ile	Gly	Arg	165	170	175	
Leu	Leu	Ala	Ala	Val	Gln	Ser	Thr	Gly	Lys	Ala	Glu	Leu	Arg	Thr	Glu	180	185	190	
Ser	Val	Leu	Thr	Ser	Leu	Ile	Val	Glu	Asp	Gly	Arg	Val	Val	Gly	Ala	195	200	205	
Glu	Val	Glu	Ser	Gly	Gly	Glu	Thr	Gln	Arg	Ile	Lys	Ala	Asn	Arg	Gly	210	215	220	
Val	Leu	Met	Ala	Ala	Gly	Gly	Ile	Glu	Gly	Asn	Ala	Glu	Met	Arg	Glu	225	230	235	240
Gln	Ala	Gly	Thr	Pro	Gly	Lys	Ala	Ile	Trp	Ser	Met	Gly	Pro	Phe	Gly	245	250	255	
Ala	Asn	Thr	Gly	Asp	Ala	Ile	Ser	Ala	Gly	Ile	Ala	Val	Gly	Gly	Ala	260	265	270	
Thr	Ala	Leu	Leu	Asp	Gln	Ala	Trp	Phe	Cys	Pro	Gly	Val	Glu	Gln	Pro	275	280	285	
Asp	Gly	Ser	Ala	Ala	Phe	Met	Val	Gly	Val	Arg	Gly	Gly	Leu	Val	Val	290	295	300	
Asp	Ser	Ala	Gly	Glu	Arg	Tyr	Leu	Asn	Glu	Ser	Leu	Pro	Tyr	Asp	Gln	305	310	315	320
Phe	Gly	Arg	Ala	Met	Asp	Ala	His	Asp	Asp	Asn	Gly	Ser	Ala	Val	Pro	325	330	335	
Ser	Phe	Met	Ile	Phe	Asp	Ser	Arg	Glu	Gly	Gly	Gly	Leu	Pro	Ala	Ile	340	345	350	
Cys	Ile	Pro	Asn	Thr	Ala	Pro	Ala	Lys	His	Leu	Glu	Ala	Gly	Thr	Trp	355	360	365	
Val	Gly	Ala	Asp	Thr	Leu	Glu	Glu	Leu	Ala	Ala	Lys	Thr	Gly	Leu	Pro	370	375	380	
Ala	Asp	Ala	Leu	Arg	Ser	Thr	Val	Glu	Lys	Phe	Asn	Asp	Ala	Ala	Lys				

385	390	395	400
Leu Gly Val Asp	Glu Glu Phe His Arg	Gly Glu Asp Pro Tyr	Asp Ala
	405	410	415
Phe Phe Cys Pro	Pro Asn Gly Gly	Ala Asn Ala Ala	Leu Thr Ala Ile
	420	425	430
Glu Asn Gly Pro	Phe Tyr Ala Ala	Arg Ile Val Leu	Ser Asp Leu Gly
	435	440	445
Thr Lys Gly Gly	Leu Val Thr Asp	Val Asn Gly Arg	Val Leu Arg Ala
	450	455	460
Asp Gly Ser Ala	Ile Asp Gly Leu Tyr	Ala Ala Gly Asn Thr	Ser Ala
	465	470	475
Ser Leu Ser Gly	Arg Phe Tyr Pro	Gly Pro Gly Val	Pro Leu Gly Thr
	485	490	495
Ala Met Val Phe	Ser Tyr Arg Ala	Ala Gln Asp Met	Ala Lys
	500	505	510

<210> 3
 <211> 158
 <212> DNA
 <213> Rhodococcus erythropolis

<400> 3
 atcatcgatt atgtgtcccg gccgcgaacg accgcgctaa ttctctcacc tggaccaccc 60
 atctcggcat attgcccgcct cagtgggacc tggcatggcc ttccagtgcc gtgcgggtatt 120
 ccgtggacac cccaccctct tggagtaagg acgcaatg 158

<210> 4
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 4
 ggcgacgttg ccgagaatt 19

<210> 5
 <211> 624
 <212> DNA
 <213> Rhodococcus erythropolis

<220>
 <221> CDS
 <222> (1)..(624)

<400> 5
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 Met Gly Ala Thr Leu Pro Arg Ile Ala Glu Val Arg Asp Ala Ala Glu

1	5	10	15	
ccc agt tcg gac gag cag cgg gcg cgc cat gtg cgg atg ctg gaa gcg	96			
Pro Ser Ser Asp Glu Gln Arg Ala Arg His Val Arg Met Leu Glu Ala				
20 25 30				
gcc gcc gaa ttg ggg acc gag aaa gaa ctc tca cgg gtt cag atg cac	144			
Ala Ala Glu Leu Gly Thr Glu Lys Glu Leu Ser Arg Val Gln Met His				
35 40 45				
gaa gtt gcc aag cgg gca ggc gtg gcc atc ggc act ctc tac cgc tat	192			
Glu Val Ala Lys Arg Ala Gly Val Ala Ile Gly Thr Leu Tyr Arg Tyr				
50 55 60				
ttc cct tcg aag acg cac ctc ttc gtc gct gtg atg gtc gag cag atc	240			
Phe Pro Ser Lys Thr His Leu Phe Val Ala Val Met Val Glu Gln Ile				
65 70 75 80				
gat cag atc ggc gac agt ttc gcc aag cat cag gtg cag tcg gcc aat	288			
Asp Gln Ile Gly Asp Ser Phe Ala Lys His Gln Val Gln Ser Ala Asn				
85 90 95				
ccg cag gac gcc gtg tac gag gtc ctg gtg cgc gcg act cgc ggg tta	336			
Pro Gln Asp Ala Val Tyr Glu Val Leu Val Arg Ala Thr Arg Gly Leu				
100 105 110				
ctg cgt cgg ccg gcc ctt tcg act gcg atg ctg cag tcg tcc agt acc	384			
Leu Arg Arg Pro Ala Leu Ser Thr Ala Met Leu Gln Ser Ser Ser Thr				
115 120 125				
gcc aac gtc gcg acg gtg ccg gac gtg ggc aag atc gat cgc ggc ttc	432			
Ala Asn Val Ala Thr Val Pro Asp Val Gly Lys Ile Asp Arg Gly Phe				
130 135 140				
cgg cag atc atc ctc gat gcg gcc ggg atc gag aac ccg acc gag gaa	480			
Arg Gln Ile Ile Leu Asp Ala Ala Gly Ile Glu Asn Pro Thr Glu Glu				
145 150 155 160				
gac aac acc ggg ttg cgt ctg ctg atg cag ctg tgg ttc ggg gtc atc	528			
Asp Asn Thr Gly Leu Arg Leu Leu Met Gln Leu Trp Phe Gly Val Ile				
165 170 175				
caa tcg tgc ctc aac ggt cga att tcc atc ccg gat gcg gag tac gac	576			
Gln Ser Cys Leu Asn Gly Arg Ile Ser Ile Pro Asp Ala Glu Tyr Asp				
180 185 190				
atc cgc aag ggg tgc gac ctg ctt ctg gtg aat ctc tca cga cac tga	624			
Ile Arg Lys Gly Cys Asp Leu Leu Leu Val Asn Leu Ser Arg His				
195 200 205				

<210> 6

<211> 207

<212> PRT

<213> Rhodococcus erythropolis

<400> 6

Met Gly Ala Thr Leu Pro Arg Ile Ala Glu Val Arg Asp Ala Ala Glu
1 5 10 15

Pro Ser Ser Asp Glu Gln Arg Ala Arg His Val Arg Met Leu Glu Ala

20										25										30														
Ala	Ala	Glu	Leu	Gly	Thr	Glu	Lys	Glu	Leu	Ser	Arg	Val	Gln	Met	His																			
		35					40					45																						
Glu	Val	Ala	Lys	Arg	Ala	Gly	Val	Ala	Ile	Gly	Thr	Leu	Tyr	Arg	Tyr																			
	50					55					60																							
Phe	Pro	Ser	Lys	Thr	His	Leu	Phe	Val	Ala	Val	Met	Val	Glu	Gln	Ile																			
65					70					75					80																			
Asp	Gln	Ile	Gly	Asp	Ser	Phe	Ala	Lys	His	Gln	Val	Gln	Ser	Ala	Asn																			
			85					90						95																				
Pro	Gln	Asp	Ala	Val	Tyr	Glu	Val	Leu	Val	Arg	Ala	Thr	Arg	Gly	Leu																			
		100					105						110																					
Leu	Arg	Arg	Pro	Ala	Leu	Ser	Thr	Ala	Met	Leu	Gln	Ser	Ser	Ser	Thr																			
	115					120					125																							
Ala	Asn	Val	Ala	Thr	Val	Pro	Asp	Val	Gly	Lys	Ile	Asp	Arg	Gly	Phe																			
	130				135					140																								
Arg	Gln	Ile	Ile	Leu	Asp	Ala	Ala	Gly	Ile	Glu	Asn	Pro	Thr	Glu	Glu																			
145				150					155					160																				
Asp	Asn	Thr	Gly	Leu	Arg	Leu	Leu	Met	Gln	Leu	Trp	Phe	Gly	Val	Ile																			
			165				170						175																					
Gln	Ser	Cys	Leu	Asn	Gly	Arg	Ile	Ser	Ile	Pro	Asp	Ala	Glu	Tyr	Asp																			
		180					185					190																						
Ile	Arg	Lys	Gly	Cys	Asp	Leu	Leu	Leu	Val	Asn	Leu	Ser	Arg	His																				
	195					200					205																							

<210> 7
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 7
 tcagtgtcgt gagagattca

20

<210> 8
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 8
 ataaagctta tcgattatgt gtcccggccg cgaac

35

<210> 9

<211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 9
 ataggtacca tatgtgcgtc cttactccaa gaggg 35

<210> 10
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 10
 gcgcatatgg ctaagaatca ggcaccc 27

<210> 11
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 11
 gcgggatccc tacttctctg ctgcgtgatg 30

<210> 12
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 12
 ggccatatgt tgaccacaga cgtgacgacc 30

<210> 13
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 13
 gccactagtt cactgcgctg ctctgcacg 30